

SEQUENCE LISTING

(1) GENERAL INFORMATION

(I) APPLICANTS:

Lenting, Hermanus Bernardus Maria  
Van Beekhoven, Rudolf Franciscus Wilhelmus Cornelis  
Maurer, Karl-Heinz  
Kottwitz, Beatrix  
Weiss, Albrecht  
Van Solingen, Pieter

(ii) TITLE OF INVENTION:

Detergents Comprising Cellulases

(iii) NUMBER OF SEQUENCES:

Two

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Henkel Corporation  
(B) STREET: 140 Germantown Pike, Suite 150  
(C) CITY: Plymouth Meeting  
(D) STATE: Pennsylvania  
(E) COUNTRY: U.S.A.  
(F) ZIP: 19462

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" diskette  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: MS-DOS  
(D) SOFTWARE: MS Word 6.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
U.S. Ser. No. 08/945,574  
(B) FILING DATE:  
unavailable  
(C) CLASSIFICATION: (IPC)  
C12N 9/42  
C11D 3/386

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBERS:  
PCT/EP96/01755  
EP 95201115.3  
U.S. 614,115  
(B) FILING DATES:  
26 Apr. 1996  
28 Apr. 1995  
12 Mar. 1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Murphy, Glenn E. J.
- (B) REGISTRATION NUMBER: 33,539
- (C) REFERENCE/DOCKET NUMBER: H 1920 PCT/US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (610) 832-2228
- (B) TELEFAX: (610) 941-6067
- (C) E-MAIL: Glenn.Murphy @ Henkel-Americas.com

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(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

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Met	Lys	Lys	Ile	Thr	Thr	Ile	Phe	Ala	Val	Leu	Leu	Met	Thr	Leu	Ala	
-26	-25						-20					-15				
Leu	Phe	Ser	Ile	Gly	Asn	Thr	Thr	Ala	Ala	Asp	Asp	Tyr	Ser	Val	Val	
-10					-5					1				5		
Glu	Glu	His	Gly	Gln	Leu	Ser	Ile	Ser	Asn	Gly	Glu	Leu	Val	Asn	Glu	
			10					15					20			
Arg	Gly	Glu	Gln	Val	Gln	Leu	Lys	Gly	Met	Ser	Ser	His	Gly	Leu	Gln	
		25					30					35				
Trp	Tyr	Gly	Gln	Phe	Val	Asn	Tyr	Glu	Ser	Met	Lys	Trp	Leu	Arg	Asp	
	40					45					50					
Asp	Trp	Gly	Ile	Thr	Val	Phe	Arg	Ala	Ala	Met	Tyr	Thr	Ser	Ser	Gly	
55					60					65					70	
Gly	Tyr	Ile	Asp	Asp	Pro	Ser	Val	Lys	Glu	Lys	Val	Lys	Glu	Thr	Val	
			75						80					85		
Glu	Ala	Ala	Ile	Asp	Leu	Gly	Ile	Tyr	Val	Ile	Ile	Asp	Trp	His	Ile	
			90					95					100			
Leu	Ser	Asp	Asn	Asp	Pro	Asn	Ile	Tyr	Lys	Glu	Glu	Ala	Lys	Asp	Phe	
		105					110					115				
Phe	Asp	Glu	Met	Ser	Glu	Leu	Tyr	Gly	Asp	Tyr	Pro	Asn	Val	Ile	Tyr	
	120					125					130					
Glu	Ile	Ala	Asn	Glu	Pro	Asn	Gly	Ser	Asp	Val	Thr	Trp	Asp	Asn	Gln	
135				140					145					150		
Ile	Lys	Pro	Tyr	Ala	Glu	Glu	Val	Ile	Pro	Val	Ile	Arg	Asp	Asn	Asp	
			155					160					165			
Pro	Asn	Asn	Ile	Val	Ile	Val	Gly	Thr	Gly	Thr	Trp	Ser	Gln	Asp	Val	
		170					175						180			
His	His	Ala	Ala	Asp	Asn	Gln	Leu	Ala	Asp	Pro	Asn	Val	Met	Tyr	Ala	
	185					190						195				

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B

Phe His Phe Tyr Ala Gly Thr His Gly Gln Asn Leu Arg Asp Gln Val  
 200 205 210  
 Asp Tyr Ala Leu Asp Gln Gly Ala Ala Ile Phe Val Ser Glu Trp Gly  
 215 220 225 230  
 Thr Ser Ala Ala Thr Gly Asp Gly Gly Val Phe Leu Asp Glu Ala Gln  
 235 240 245  
 Val Trp Ile Asp Phe Met Asp Glu Arg Asn Leu Ser Trp Ala Asn Trp  
 250 255 260  
 Ser Leu Thr His Lys Asp Glu Ser Ser Ala Ala Leu Met Pro Gly Ala  
 265 270 275  
 Asn Pro Thr Gly Gly Trp Thr Glu Ala Glu Leu Ser Pro Ser Gly Thr  
 280 285 290  
 Phe Val Arg Glu Lys Ile Arg Glu Ser Ala Ser Ile Pro Pro Ser Asp  
 295 300 305 310  
 Pro Thr Pro Pro Ser Asp Pro Gly Glu Pro Asp Pro Gly Glu Pro Asp  
 315 320 325  
 Pro Thr Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn  
 330 335 340  
 Gln Ile Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln  
 345 350 355  
 Ala Lys Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro  
 360 365 370  
 Trp Glu Pro Leu Lys Ser Asp Pro Asp Ser Gly Glu Pro Asp Pro Thr  
 375 380 385 390  
 Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn Gln Ile  
 395 400 405  
 Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln Ala Lys  
 410 415 420  
 Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro Trp Glu  
 425 430 435  
 Pro Leu Asn  
 440

(3) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

B3

Met	Lys	Trp	Met	Lys	Ser	Met	Val	Trp	Leu	Ala	Val	Val	Leu	Val	Val	
1				5					10					15		
Ser	Phe	Val	Ala	Pro	Ala	Val	Ser	Ser	Ala	Asn	Glu	Asp	Val	Lys	Thr	
			20					25					30			
Leu	Asp	Ile	Gln	Ser	Tyr	Val	Arg	Asp	Met	Gln	Pro	Gly	Trp	Asn	Leu	
	35						40					45				
Gly	Asn	Thr	Phe	Asp	Ala	Val	Gly	Gln	Asp	Glu	Thr	Ala	Trp	Gly	Asn	
	50					55					60					
Pro	Arg	Val	Thr	Arg	Glu	Leu	Ile	Glu	Arg	Ile	Ala	Asp	Glu	Gly	Tyr	
65					70					75					80	
Lys	Ser	Ile	Arg	Ile	Pro	Val	Thr	Trp	Glu	Asn	Arg	Ile	Gly	Gly	Ala	
			85						90					95		
Pro	Asp	Tyr	Pro	Ile	Asp	Pro	Gln	Phe	Leu	Asn	Arg	Val	Asp	Glu	Val	
			100					105					110			
Val	Gln	Trp	Ala	Leu	Glu	Glu	Asp	Leu	Tyr	Val	Met	Ile	Asn	Leu	His	
	115						120					125				
His	Asp	Ser	Trp	Leu	Trp	Ile	Tyr	Glu	Met	Glu	His	Asn	Tyr	Asn	Gly	
	130					135					140					
Val	Met	Ala	Lys	Tyr	Arg	Ser	Leu	Trp	Glu	Gln	Leu	Ser	Asn	His	Phe	
145					150					155					160	
Lys	Asp	Tyr	Pro	Thr	Lys	Leu	Met	Phe	Glu	Ser	Val	Asn	Glu	Pro	Lys	
			165						170					175		
Phe	Ser	Gln	Asn	Trp	Gly	Glu	Ile	Arg	Glu	Asn	His	His	Ala	Leu	Leu	
			180					185					190			
Asp	Asp	Leu	Asn	Thr	Val	Phe	Phe	Glu	Ile	Val	Arg	Gln	Ser	Gly	Gly	
	195						200					205				
Gln	Asn	Asp	Ile	Arg	Pro	Leu	Val	Leu	Pro	Thr	Met	Glu	Thr	Ala	Thr	
	210					215					220					

Ser Gln Pro Leu Leu Asn Asn Leu Tyr Gln Thr Ile Asp Lys Leu Asp  
 225 230 235 240  
 Asp Pro Asn Leu Ile Ala Thr Val His Tyr Tyr Gly Phe Trp Pro Phe  
 245 250 255  
 Ser Val Asn Ile Ala Gly Tyr Thr Arg Phe Glu Glu Asp Ser Lys Arg  
 260 265 270  
 Glu Ile Ile Glu Thr Phe Asp Arg Val His His Thr Phe Val Ala Arg  
 275 280 285  
 Gly Ile Pro Val Val Leu Gly Glu Phe Gly Leu Leu Gly Phe Asp Lys  
 290 295 300  
 His Thr Gly Val Ile Gln Gln Gly Glu Lys Leu Lys Phe Phe Glu Tyr  
 305 310 315 320  
 Leu Ile His His Leu Asn Glu Arg Asp Ile Thr His Met Leu Trp Asp  
 325 330 335  
 Asn Gly Gln His Phe Asn Arg His Thr Tyr Glu Trp Tyr Asp Glu Glu  
 340 345 350  
 Leu Phe Asp Met Leu Arg Ala Ser Trp Gly Gly Arg Ser Ser Val Ala  
 355 360 365  
 Glu Ser Asn Phe Ile Tyr Leu Lys Gln Gly Asp Arg Ile Ala Asp Ala  
 370 375 380  
 Thr Val Thr Leu Gln Leu His Gly Asn Glu Leu Thr Gly Leu Gln Ala  
 385 390 395 400  
 Asn Gly Gln Arg Leu Thr Pro Gly Gln Asp Tyr Glu Leu Asn Gly Glu  
 405 410 415  
 Arg Leu Thr Val Lys Ala His Val Leu Ser Ala Ile Ala Gly Ser Gly  
 420 425 430  
 Thr Leu Gly Thr Asn Gly Met Val Thr Ala Glu Phe Asn Arg Gly Ala  
 435 440 445  
 Asp Trp His Phe Arg Val Asn Thr Tyr Arg Thr Pro Val Leu Gln Ser  
 450 455 460  
 Thr Gln Gly His Val Ser Asn Phe Ser Ile Pro Ala Ser Phe Asn Gly  
 465 470 475 480  
 Asn Ser Leu Ala Thr Met Glu Ala Val Tyr Val Asp Gly Gly Asn Ala  
 485 490 495  
 Gly Pro Gln Asp Trp Thr Ser Phe Lys Glu Phe Gly Tyr Ala Phe Ser  
 500 505 510

Pro Ser Tyr Asp Thr His Glu Ile Lys Leu Thr Glu Ala Phe Phe Arg  
515 520 525

Glu Val Arg Asp Gly Glu Val Arg Leu Thr Phe His Phe Trp Ser Gly  
530 535 540

B3 Glu Ile Val Asn Tyr Thr Ile Ile Lys Asn Gly Asn Gln Val Thr Gly  
545 550 555 560

Ile Ala Ala Gln Thr Thr Asn Ser Lys Asn Lys Asn Lys Lys  
565 570

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